

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: August 13, 2002, 17:36:08 ; Search time 1833.38 Seconds
(without alignments)
11425.598 Million cell updates/sec

Title: US-09-761-580-1_COPY_800_1800
Perfect score: 1001
Sequence: 1 atatatacagcatgttgcac.....cagtggaggccagggttt 1001
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1797656 seqs, 10463268293 residues
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_htc:
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4: gb_com:
5: gb_ov:
6: gb_pat:
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8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sty:
13: gb_un:
14: gb_vl:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
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22: em_lov:
23: em_pat:
24: em_lph:
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26: em_ro:
27: em_ls19:
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29: em_htg_hum:
30: em_htg_inv:
31: em_htg_other:
32: em_htg_inv:
33: em_htg_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|-------------|
| | | | | SUMMARIES |

ALIGMENTS

| RESULT | 1 | AX151744 | AX151744 | 2583 bp | DNA | linear | PAT 22-JUN-2001 |
|------------|---|----------|----------|---|-----|--------|-----------------|
| LOCUS | | | | Sequence 1 from Patent | | | |
| DEFINITION | | | | EP118679. | | | |
| ACCESSION | | | | AX151744 | | | |
| VERSION | | | | AX151744.1 | | | |
| KEYWORDS | | | | GT:14533673 | | | |
| SOURCE | | | | . | | | |
| ORGANISM | | | | Homo sapiens | | | |
| REMARKS | | | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. | | | |
| REFERENCES | | | | 1. (bases 1 to 2583) | | | |
| AUTHORS | | | | Smith,J.C., Arand,R. and Morten,J.E. | | | |
| TITLE | | | | Method for diagnosing polymorphisms in the human pdh e2 gene | | | |
| JOURNAL | | | | Patent: EP 118679-A 1 25-JUL-2001; Astrazeneca AB (SE) | | | |
| FEATURES | | | | Location/Qualifiers | | | |
| source | | | | 1. /organism="Homo sapiens" | | | |
| BASE COUNT | | | | /db_xref="Taxon:9606" | | | |
| ORIGIN | | | | /db_xref="Taxon:9606" | | | |


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Best Local Similarity 91.9%; Pred. No. 1-1e-202;
Matches 920; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
RESULT      6
AY044265
LOCUS    AY044265
1700 bp mRNA linear ROD 01-NOV-2001

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RESULT 9
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LOCUS D00092 N00092
DEFINITION Rattus norvegicus mRNA for 70 kd mitochondrial autoantigen, partial cds.
ACCESSION D00092.1 GI:2951761
VERSION 70 kd mitochondrial autoantigen.
KEYWORDS Rattus norvegicus liver cDNA to mRNA, clone lib:cDNA library in lambda gt1-Amp3, provided by Dr. Geoffrey Howlett sub_clone:PRMT.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
MATERIALS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE (bases 1 to 1370)
AUTHORS Gershwin,M.E., Mackay,I.R., Sturges,A. and Coppel,R.L.
TITLE Identification and specificity of a cDNA encoding the 70 kd mitochondrial antigen recognized in primary biliary cirrhosis
JOURNAL J. Immunol. 138 (10), 3525-3531 (1987)
MEDLINE 8719638
COMMENT On Mar 11, 1998 this sequence version replaced 91:220817.
 They report the identification of a cDNA clone derived from a rat liver gene expression library that expresses the 70 kd mitochondrial autoantigen of primary biliary cirrhosis (PBC). The sequence does not correspond to any known protein and is encoded by nuclear DNA.
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 /sub_clone="PRMT"
 /tissue_type="liver"
 /clone_lib="cDNA library in lambda gt1-Amp3, provided by Dr. Geoffrey Howlett"
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 /codon_start=1
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 BASE COUNT 368 a 348 c 335 g 319 t
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 best local Similarity 85.6%; Pred. No. 1.5e-169;
 Matches 839; Conservative 0; Mismatches 127; Indels 17; Gaps 3;
QY 1 attatccatcgatttgcgactataggccaaacggaaatccggatttaaaccaccaatgc 60
DB 380 ATTAAGACGACATGGCACTTCAGCCACAGGCACCTGTTCCTCCATGCCAGCTTAACGCCACGGCA 439
QY 61 caccacccatccccccatggggctgttccaaactcccccggatccatgtttagctca 120
DB 440 CACCACTGTCACCCCGAAGGGCACTGTTCCTCCATGCCAGCTTAACGCCACGGCA 499
QY 121 cacccatcgacccatgtcccaatccggatctgttgaccaaaaggaaagggttttgttagcc 180
DB 500 CCC-----CTTACGGCCRCCTGCTGGACCAAAGGGAAGGGTGTGCTGATGCC 547
QY 181 ctctggcaagaaggatggcagtagagaaaggatgtttcacacgttaaaggacac 240
DB 548 CTCTGGCAAGAGATTGGCAGGAGAAGGGATCTACCCGAGTAAAGGACGG 607

| | REFERENCE |
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| ORIGIN | Mammalia; <i>Buttereria</i> ; Rodentia; <i>Sciurognathi</i> ; Muridae; Murinae; <i>Mus</i> . /codon_start=1 /product="dihydroliptopamide S-acetyltransferase." /protein_id="CAA3202.1" /db_xref="GI:310524" /db_xref="SPTREMBL:001991" /translation="RPTSSAPCPRTPAGPKGRVESPPLAKKLAVERKGIDLTQVKGTP DGRITKQIDSFSVSKVARAPAAVVPPIPGMAVPTGFTDIPSNIRVIARLMO SKOPIPHYLSDIDVNMGELVLVRLENLKLEGRSKISVNDIFIKRSALACKVPEANS SWMDTIVRNHVVVDVSVAVSTPAGLITPVENAHIKGVETIANDVVSLATKARECKLQ |
| BASE COUNT | 200 a 140 c 143 g 177 t |
| Query Match | 65.5%; Score 655.8; DB 9; Length 660; |
| Best Local Similarity | 99.7%; Pred. No. 5.4e-150; |
| Matches | 637; Conservative 0; Mismatches 2; Indels 0; Gaps 0; |
| Ov | 115 ctccatcacacttcgcacccgtccggccacgtctccgtggaccacaaggaaaggat 174 2 CTCACACTTCAGCACCCGTGCCAGCTACTCCTCGTGGACCACAGGGTTG 61 |
| Qy | 175 tttagccctcttgcaagaacttggaaataagaaggatgatcttacccaagaaagg 234 62 TTAGCCTCTTGCAALAGAAGTGGCGTAGAGAAAGGATGATCAGTAAG 121 |
| Oy | 235 ggacaggaccaggatgttagatcacaaggagatcgcgtttgtggcttagtaag 294 Db 122 GGACAGGACGACAGATGTAGATCACCAGAGGATATCGACHTTGTGCCTAGAAG 181 |
| Oy | 295 ttgtccctgtccggcagctttgtggccctccacaggctccggaaatggcaccagtcc 354 Db 182 TTGCCRCTGTCGGCAGCTGGTGGCTCCACAGTCUGGAANGGCACAGTCTTA 241 |
| Oy | 355 cagggtgtttcacatcatccaaatcggacacattcggtgggttatggcagcggattaa 414 Db 242 CAGGCTCTTCACGATATGCCAACGACATTCGCGGTTATGCCAGGGTTA 301 |
| Oy | 415 tgcatacaaggaaaccatcttcattatctttttatcgatqtaaatatgggaaag 474 Db 302 TGCAATCAAGCAACCATACCTCTTATTAATCTTGATGTAATAATTGGGAGAG 361 |
| Oy | 475 tttttttggcgggaaacttaataaaatggatattaaaggaaacaaatttcgtca 534 Db 362 TTTTGTGGTGGAGGGAAAGACTTAATAGATTTAGAGGGAGGAAATTCGTCA 421 |
| Oy | 535 atgacttcataaaaatggctcaagttggatgtttaaatggaaatggaaatctt 594 422 ATGACTTCATATAAACGTCAGCTTGGTAAGTCCCGAACAAATCTT 481 |
| FEATURES | BASE COUNT |
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| /codon_start=3 | /product="unn known (protein for IMAGE:3586777)" /protein_id="NAH0202.1" /db_xref="GI:13309818" |
| /translation="HASAHIGLEITIASDWVSLASKAREGKLOPHEFOGGFTTISNLG MFGIAKNSLNINPQACILAGASSEDKLIPADNEKGDFDVSVSNTLSODHRVVDGAV GAQMLAEPRKYLEPITML" | |
| ORIGIN | 632 a 369 c 419 g 618 t |
| RESULT | 13 |
| BC003202 | BC003202 2038 bp mRNA linear ROD 12-JUL-2001 |
| LOCUS | Mus musculus, clone IMAGE:3586777, mRNA, partial cds. |
| DEFINITION | |
| ACCESSION | BC003202 |
| VERSION | BC003202.1 GI:13096817 |
| KEYWORDS | house mouse. |
| SOURCE | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |

Search completed: August 13, 2002, 19:30:33
Job time: 6865 sec

OM nucleic - nucleic search, using sw model
Run on: August 13, 2002, 18:26:23 ; Search time 208.64 Seconds
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ALIGNMENTS

RESULT 1
AAD07345
ID AAD0745 **standard:** DNA; 2583 BP.
AC
XX
DP 12-SEP-2001 **(first entry)**
DE Human pyruvate dehydrogenase complex E2 (PDPH E2 or PDC E2) gene.
XX
KW Human; pyruvate dehydrogenase complex E2; PDPH E2; PDC E2; Polymorphism;
KW lactic acidemia; coronary failure; cardiac myopathy; weakness; diabetes;
KW muscle ataxia; peripheral vascular disease; myocardial ischaemia; asthma;
KW bioinformatic analysis; pharmacogenetic analysis; obesity; sepsis; drug;
KW genetic marker; therapy; ds.
XX
OS Homo sapiens.
XX
FH location/Qualifiers
FT 211..1848
FT CDS
FT /*tag= a
FT /product= "Human pyruvate dehydrogenase complex E2"
FT replace (857, C)
FT /*tag= c
FT /note= "This variation occurs during polymorphism"
FT replace (1255, A)
FT /*tag= d
FT /note= "This variation occurs during polymorphism"
PN EP1118679-A1.
XX
XX
PD 25-JUL-2001.

QY 573 aaagtccggcgaattcttcgtggaggaccatgtataacaatcatgttt 632
 Db 1023 aagttcccgaaatccgcctgatggacatgttcaagacgacgacgtc 1082
 QY 633 gagtcgttccgttccgtactctggaggactatcacccatgtttatgg 692
 Db 1083 gagtttccgtgtgtccacagacaaggctgtatccccgatgtttccatgg 1142
 QY 693 catataaaggatggagaccatgtataatgtatgttttttgcacaaaga 752
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 QY 753 gaggttataactacggccatgtatccgggtggacttttacatctcaattaga 812
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 QY 813 aqgtttggaaattttagaattttctctgtatattaaacctcaacgttgc 872
 -- 1263 atgttcgtgtgaaaccatgttgcggctgtatcaacccctcaatcgatcttgc 1322
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 QY 930 gctggatgttactgttactgttactgtgtatccgggtggatggacgttga 989
 Db 1383 gtcaacatgtgtggatgttactgtgtatccgggtggatggatgtgtgtct 1442
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 Db 1443 gccagggtgtt 1453

RESULT B
 ABL09105 standard; cDNA; 1850 BP.
 ID ABL09105;
 AC XX
 XX
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 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21797.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 WO2017042-A2.
 ^X
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PT Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI: 2001-656800/75.
 DR P-PSDB; ABB65002.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
 PS Claim 1; SEQ ID NO 21797; 21pp + Sequence Listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and

SQ CC cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB11676-AB130511), expressed DNA sequences (AB101840-ABL16175) and the encoded proteins (ABB7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

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| PR | 06-MAY-1999; | 99US-0132486. | PR | 22-JUL-1999; | 99US-0145089. |
| PR | 07-MAY-1999; | 99US-0132487. | PR | 22-JUL-1999; | 99US-0145192. |
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| PR | 14-MAY-1999; | 99US-0134219. | PR | 26-JUL-1999; | 99US-0145276. |
| PR | 14-MAY-1999; | 99US-0134221. | PR | 27-JUL-1999; | 99US-0145913. |
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| PR | 07-JUN-1999; | 99US-0137724. | PR | 06-AUG-1999; | 99US-0147116. |
| PR | 08-JUN-1999; | 99US-0138094. | PR | 09-AUG-1999; | 99US-0147493. |
| PR | 10-JUN-1999; | 99US-0138540. | PR | 09-AUG-1999; | 99US-0147935. |
| PR | 10-JUN-1999; | 99US-0138847. | PR | 10-AUG-1999; | 99US-0148171. |
| PR | 14-JUN-1999; | 99US-0139119. | PR | 11-AUG-1999; | 99US-0148319. |
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| PR | 21-JUN-1999; | 99US-0139817. | PR | 27-AUG-1999; | 99US-0151066. |
| PR | 22-JUN-1999; | 99US-0139839. | PR | 27-AUG-1999; | 99US-0151080. |
| PR | 23-JUN-1999; | 99US-0140353. | PR | 30-AUG-1999; | 99US-0151303. |
| PR | 23-JUN-1999; | 99US-0140354. | PR | 31-AUG-1999; | 99US-0151438. |
| PR | 24-JUN-1999; | 99US-0140635. | PR | 01-SEP-1999; | 99US-0151930. |
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| PR | 01-JUL-1999; | 99US-0141842. | PR | 15-SEP-1999; | 99US-0154018. |
| PR | 02-JUL-1999; | 99US-0142154. | PR | 16-SEP-1999; | 99US-0154039. |
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| PR | 14-JUL-1999; | 99US-0143634. | PR | 29-SEP-1999; | 99US-0156596. |
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| PR | 16-JUL-1999; | 99US-0144333. | PR | 05-OCT-1999; | 99US-0157753. |
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| PR | 19-JUL-1999; | 99US-0144335. | PR | 08-OCT-1999; | 99US-0158232. |
| PR | 20-JUL-1999; | 99US-0144335. | PR | 12-OCT-1999; | 99US-0158369. |
| PR | 20-JUL-1999; | 99US-0144335. | PR | 13-OCT-1999; | 99US-0158373. |
| PR | 20-JUL-1999; | 99US-0144884. | PR | 13-OCT-1999; | 99US-0159294. |
| PR | 21-JUL-1999; | 99US-0144884. | PR | 18-OCT-1999; | 99US-0159329. |
| PR | 21-JUL-1999; | 99US-0145086. | PR | 14-OCT-1999; | 99US-0159330. |
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| PR | 21-OCT-1999; | 99US-0160815. |
| PR | 22-OCT-1999; | 99US-0160880. |
| PR | 22-OCT-1999; | 99US-0160881. |
| PR | 22-OCT-1999; | 99US-0160889. |
| PR | 25-OCT-1999; | 99US-016104. |
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| PR | 26-OCT-1999; | 99US-016159. |
| PR | 26-OCT-1999; | 99US-0161360. |
| PR | 26-OCT-1999; | 99US-0161361. |
| PR | 28-OCT-1999; | 99US-0161920. |
| PR | 28-OCT-1999; | 99US-0161992. |
| PR | 28-OCT-1999; | 99US-0161993. |
| PR | 29-OCT-1999; | 99US-0162142. |

AAS92326; standard; cDNA; 2595 BP.
ID AAS92326
XX
AC
XX

| | | |
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| DE | 13-FEB-2002 | (first entry) |
| XX | DN | encoding novel human diagnostic protein #28130. |
| XX | KW | Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss. |
| XX | OS | Homo sapiens. |
| XX | PN | W020175067-A2. |
| PD | 11-OCT-2001. | |
| XX | PP | 30-MAR-2001; 2001WO-US08631. |
| XX | PR | 31-MAR-2000; 2000US-0540217. |
| PR | 23-AUG-2000; 2000US-0649167. | |
| XX | PA | (HYSEQ) HYSEQ INC. |
| XX | PI | Drmancic RT, Liu C, Tang YT; |
| XX | DR | WIPO; 2001-639362/73. |
| DR | PT | P-FSDB; ABG28139. |
| XX | XX | New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity. |
| PS | Claim 1; SEQ ID No 28130; 103pp; English. | |
| XX | CC | The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (III). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against (I), detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS6A197-AAS94564 represent novel human diagnostic coding sequences of the invention. |
| CC | CC | Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.Wipo.int/pub/published_pet_sequences . |
| CC | SQ | Sequence 2595 BP; 967 A; 505 C; 551 G; 572 T; 0 other: |
| CC | Query Match 9.7%; Score 96.6; DB 23; Length 2595; Best Local Similarity 91.9%; Pred. No. 2; 8e-17; Matches 102; Conservative 0; Mismatches 9; Indels 0; Gaps 0; | |
| CC | QY 303 gtcggcgacgttggcgctccacgggtttggatggaccgttccacaggtgc 362 1535 gtcggcgacgttggcgctccacagggtttggatggaccgttccacaggtgc 1476 | |
| QY 363 ttccacatattccaaatcagaacatcgccgggttattggacagatgttgc 413 Db 1475 ttccacatattccaaatcagaacatcgccgggttattggacagatgttgc 1425 | | |
| RESULT 14 | AA81500 | AA81500 standard; DNA: 22863 BP. |
| ID | AA81500 | |

Search completed: August 13, 2002, 19:38:36
Job time: 4333 sec

Query Match 6.2%; Score 62.2; DB 4; Length 1039;
 Best Local Similarity 47.8%; Pred. No. 6.4e-09; Gaps 0;
 Matches 181; Conservative 0; Mismatches 198; Index 0; Gaps 0;

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| QY | 586 caaatcttcgttggatggacacagtataagacaatccatgttgtatgtcaatgg 645 |
| Db | 3897 TGAACCTCTATCAGCGGCAATGCTTACCCACATTTCGAGGCAGATCG 3956 |
| QY | 646 cggtcgtactctcgaggatcatcacacctattatgtttatgcacatataaaagg 705 |
| Db | 3957 CGGTCTACTGGCCGGCCGGCTCGGATGCGATACCTCGCA 4016 |
| QY | 706 tggaaacctatgtaatgtatgtttttatgcacatataaaagg 765 |
| Db | 4017 TGGCAGACATGAGAAATCAAAGAGCTGGCAGICAAAGCCGGACGGCAAGCTGA 4076 |
| QY | 766 agccacatgttccagggtggactttatgcacatataaaagg 825 |
| Db | 4077 CGGTGAGATCTGACGGGTGTACTTCATCACACGGTGGTGTTGRC 4136 |
| QY | 826 aagaatcttcgttattatataaccacatcaatggcaatgttgcgttcgg 885 |
| Db | 4137 TGATGCTACGCCGATCATACCCGGCCAGAGCGCAATTCGGGTATGCCAGTCA 4196 |
| QY | 886 aggataactgttccatggatgtttttatgcacatataaaagg 945 |
| Db | 4197 AGATCGTCGATGGGGTGAATGGICA-----GGTAGATCTGGCGAATGATGAC 4250 |
| QY | 946 ttacactcgtgtatcacccgggtgtatgg 979 |
| Db | 4251 TGGCGCTCTACGATCACCGCTGATGCG 4284 |

RESULT 7
 US-08-975-762-36
 Sequence 36, Application US/08975762
 Patent No. 6207169

GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond

APPLICANT: Seed and BERRY LLP

ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/975,762
 FILING DATE: 21-MAR-1997
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.439

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-622-4900
 TELEFAX: 206-622-6031
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1039 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE: Ehrlichia
 ORGANISM: Ehrlichia

RESULT 7
 US-08-975-762-36
 Sequence 36, Application US/08975762
 Patent No. 6207169

GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond

APPLICANT: Seed and BERRY LLP

ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/975,762
 FILING DATE: 21-MAR-1997
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.439

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-622-4900
 TELEFAX: 206-622-6031
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1039 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

RESULT 8
 US-08-821-324-36
 Sequence 36, Application US/08821324
 Patent No. 6231869

GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond

APPLICANT: Seed and BERRY LLP

ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/821,324
 FILING DATE: 21-MAR-1997
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.439

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-622-4900
 TELEFAX: 206-622-6031
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1039 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

us-09-761-580-1_copy_800_1800.rni

MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Ehrlichia
 US-08-821-324-36

RESULT 13
 US-08-209-747-1/C
 Sequence 1, Application US/08209747
 Patent No. 573371
 GENERAL INFORMATION:
 APPLICANT: Colgin, Mark V.
 TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Birch, Stewart, Kolasch & Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 ZIP: 22040-3487
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/209,747
 FILING DATE: 14-MAR-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 1447-104P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-205-8000
 TELEX/FAX: 703-205-8050
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2793 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Nephila clavipes
 TISSUE TYPE: minor ampullate gland
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 183..2675
 OTHER INFORMATION: /product= "N. clavipes minor"
 OTHER INFORMATION: ampullate silk protein
 US-08-209-747-1

Query Match 4.3%; Score 42.6; DB 1; Length 2793;
 Best Local Similarity 59.5%; Pred. No. 0.0085; Matches 72; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

OY 38 aacagattaaaccaacaatggccaccatccccaccggcggtgcggcgttctcc 97
 Db 1663 ACCATATCCACCCACCGGAGCTGCACGCCAGCACGGCAACTCCAGCACC 1604
 OY 98 aactcccccacggtttagtcctacacccatggccaccatccggccatgtggacc 157
 Db 1603 AGCACCTCTACCGTAACCACCCACGGCTCCAGCTGCAGCTGCAGCACC 1544
 OY 158 a 158
 Db 1543 A 1543

RESULT 14
 US 08-298-1/C
 Sequence 1, Application US/08458298
 Patent No. 5756677
 GENERAL INFORMATION:
 APPLICANT: Lewis, Randolph V.
 TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Birch, Stewart, Kolasch & Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 ZIP: 22040-3487
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,298
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/209,747
 FILING DATE: 14-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 1447-104P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-205-8000
 TELEX/FAX: 703-205-8050
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2793 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Nephila clavipes
 TISSUE TYPE: minor ampullate gland
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 183..2675
 OTHER INFORMATION: /product= "N. clavipes minor"
 OTHER INFORMATION: ampullate silk protein
 US-08-458-298-1

Query Match 4.3%; Score 42.6; DB 1; Length 2793;
 Best Local Similarity 59.5%; Pred. No. 0.0085; Matches 72; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

OY 38 aacagattaaaccaacaatggccaccatccccaccggcggtgcggcgttctcc 97
 Db 1663 ACCATATCCACCCACCGGAGCTGCACGCCAGCACGGCAACTCCAGCACC 1604
 OY 98 aactcccccacggtttagtcctacacccatggccaccatccggccatgtggacc 157
 Db 1603 AGCACCTCTACCGTAACCACCCACGGCTCCAGCTGCAGCTGCAGCACC 1544
 OY 158 a 158
 Db 1543 A 1543

us-09-761-580-1_copy_800_1800.rni

Search completed: August 13, 2002, 19:31:35
Job time: 6827 sec

Om nucleic - nucleic search, using sw model

Run on: August 13, 2002, 17:33:53 ; search time 1695.31 Seconds
 (without alignments)
 796.311 Million cell updates/sec

Scoring table: IDENTITY_NUC Gapov 10.0 , Gapext 1.0

Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_estin:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_gss:*

13: em_gss_hum:*

14: em_gss_inv:*

15: em_gss_pn:*

16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Length | DB ID | Description |
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| 1 | 739 | 73..8 | 751 | AL040276 |
| 2 | 712.2 | 71..1 | 745 | ALB61280 |
| 3 | 685.4 | 68..5 | 738 | AU126868 |
| 4 | 682.2 | 68..2 | 833 | AU127045 |
| 5 | 630.6 | 63..0 | 673 | BG778185 |
| 6 | 630 | 62..9 | 833 | BG1092658 |
| 7 | 608.6 | 60..9 | 901 | B1730459 |
| 8 | 595 | 59..4 | 1030 | BK463514 |
| 9 | 582.4 | 58..2 | 857 | BG353201 |
| 10 | 555.6 | 55..5 | 720 | BK939962 |
| 11 | 552.8 | 55..2 | 680 | BG503419 |
| 12 | 532.4 | 53..2 | 1125 | BK390485 |
| 13 | 526 | 52..6 | 664 | BEB50747 |
| 14 | 515.4 | 51..5 | 654 | BG658188 |
| 15 | 509 | 50..8 | 774 | BEG27518 |
| 16 | 508 | 50..7 | 669 | BEG27518 |
| 17 | 473.2 | 47..3 | 828 | BF209700 |

ALIGNMENTS

| RESULT | 1 |
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| AL040276 | AL040276 DKEFP434K2113 r1 434 (synonym: htcs3) mRNA sequence. |
| LOCUS | AL040276 |
| DEFINITION | DKEFP434K2113 5' mRNA sequence. |
| ACCESSION | AL040276 |
| VERSION | AL040276.1 |
| KEYWORDS | EST |
| SOURCE | human. |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. |
| REFERENCE | 1 (bases 1 to 751) |
| AUTHORS | Koehler, K., Beyer, A., Newes, H.W., Gassenhuber, J. and Wiemann, S. |
| TITLE | EST (Koehler, et al.) |
| JOURNAL | Unpublished (1999) |
| COMMENT | Contact: Koehler K |
| MPS | Am Klopferspitz 18a D-82152 Martinsried, Germany |
| | This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project. |
| | No sl1 sequence available. |
| | This clone (DKEFP434K2113) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. |
| FEATURES | Location/Qualifiers |
| SOURCE | 1..751 |
| | /organism="Homo sapiens" |
| | /db_xref="taxon:9606" |
| | /clone="DKEFP434K2113" |
| | /clone_id="434 (synonym: htcs3)" |
| | /tissue_type="tissue" |
| | /de_stag="adult" |
| | /lab_host="DHIOB" |
| | /note="Vector: psport1; Site_1: NotI; Site_2: SalI" |

BASE COUNT

226 a 147 c 160 g 218 t

| | | | | |
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| QY | 448 | ttctatcgatgttaaatatggagaagtttgttgcgtacggaaagacttaataagat | 507 | |
| Db | 421 | TTCATCGATGAGTACATATTGGAGAG-TTCTTGTTACGGAAACTTAATAAGAT | 479 | |
| QY | 508 | tagaaggagaagaaatttctgtcaatgttcatacataaagttccatgttgcat | 567 | |
| Db | 480 | TAGAAGGGAGAACAAATTTCTGTCAATGACTTCATCATAAAGCTTCACCCCTGGCAT | 539 | |
| QY | 568 | gtttaaaggatcccgagaaattttcttttgtatggacacatgttatagaca-aatcat | 626 | |
| Db | 540 | GTTAAAGTCCGGAAGCAGTCTCTGGATGGACAGTTATAAGACACATCAT | 599 | |
| QY | 627 | gttgttca-g-ttcagcggtcgctggacttgcggacttgcggacttgcggacttgcggat | 685 | |
| Db | 600 | GTTGTCAGTGTGGCTAGTACCTCTGCAGGACTCATCACACCTATGIGT | 659 | |
| QY | 686 | taatgacatata 698 | | |
| | 660 | TTATGCACATT'A 672 | | |
| RESULT | 6 | | | |
| LOCUS | BI092658 | 833 bp mRNA linear EST 20-JUN-2001 | | |
| DEFINITION | 6028584651 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4998115' | | | |
| ACCESSION | BI092658 | | | |
| VERSION | BI092658.1 | | | |
| KEYWORDS | EST. | | | |
| SOURCE | human. | | | |
| ORGANISM | Homo sapiens | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| REFERENCE | 1 (bases 1 to 833) | | | |
| AUTHORS | NIH_MGC http://mgc.ncbi.nih.gov/. | | | |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | | |
| JOURNAL | Unpublished (1999) | | | |
| COMMENT | Contact : Robert Strausberg, Ph.D. Email: cgabps>r@mail.nih.gov | | | |
| Tissue | Procurement: ATCC | | | |
| CDNA Library Preparation: Life Technologies, Inc. | | | | |
| CDNA Library Arrayed by: Incyte Genomics, Inc. | | | | |
| DNA Sequencing by: Incyte Genomics, Inc. | | | | |
| Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: | | | | |
| http://image.llnl.gov/Plate: LIAM1030 row: k column: 12 | | | | |
| High quality sequence stop: 746. | | | | |
| ATURRS | Location/Qualifiers | | | |
| | . -833 | | | |
| | /organism="Homo sapiens" | | | |
| | /db_xref="taxon:9606" | | | |
| | /clone="IMAGE:99811" | | | |
| | /clone_id="NIH_MGC_10" | | | |
| | /cell_line="MGCB" | | | |
| | /lab_host="DH10B" | | | |
| | /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; | | | |
| | Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. | | | |
| | Average insert size 1.5 kb. Library prepared by Life | | | |
| | Technologies." | | | |
| BASE COUNT | 252 | a 162 c 173 g 246 t | | |
| ORIGIN | | | | |
| Query Match | 62.9% | Score 630; DB 10; Length 833; | | |
| Best local Similarity | 98.9% | Pred. No. 9.6e-153; | | |
| Matches | 645; | Conservative 0; Mismatches 5; Indels 2; Gaps 1; | | |
| QY | 352 | ctacagggtgtttcacagatattccaaatccagaaatccgtcggttttgtccacagat | 411 | |
| | | | | |
| Db | 1 | CTACAGGGTCTTCACAGATATCCAACTGAGCACATCTGGCTGTTATGCACTGGAT | 60 | |
| QY | 412 | taatgcaatcaaagcaaacatccatattacctttatcgatataatgggg | 471 | |
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| | /db_xref="taxon:10090" | | | |
| | /clone="IMAGE:5358430" | | | |
| | /clone_id="NIH_MGC_94" | | | |
| RESULT | 7 | | | |
| LOCUS | BT1730459 | 901 bp mRNA linear EST 20-SEP-2001 | | |
| DEFINITION | 603350793F1 NIH_MGC_94 MUS musculus cDNA clone IMAGE:5358430 5' | | | |
| ACCESSION | BT1730459 | | | |
| VERSION | BT1730459.1 | | | |
| KEYWORDS | EST. | | | |
| SOURCE | mouse. | | | |
| ORGANISM | Mus musculus | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. | | | |
| REFERENCE | 1 (bases 1 to 901) | | | |
| AUTHORS | NIH_MGC http://mgc.ncbi.nih.gov/. | | | |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | | |
| JOURNAL | Unpublished (1999) | | | |
| COMMENT | Contact : Robert Strausberg, Ph.D. Email: cgabps>r@mail.nih.gov | | | |
| Tissue | Procurement: The Cepko Laboratory | | | |
| CDNA Library Preparation: Life Technologies, Inc. | | | | |
| CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) | | | | |
| DNA Sequencing by: Incyte Genomics, Inc. | | | | |
| Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: | | | | |
| http://image.llnl.gov/Plate: LIAM1911 row: 1 column: 23 | | | | |
| High quality sequence stop: 843. | | | | |

| | | | | | | |
|------------|---|---|-----|-----|--|-----|
| | | | QY | 290 | taaqtgtctctgtccggcagctgttggtctccacacggctctgtgaatggaccagg | 349 |
| Db | 521 | CAAAGCAAAACCATACCTCATATTACCTGTTCTGATGTAATATGGAGAAGTTCG | 580 | | | |
| OY | 480 | tgcgtacggaaagacttaataagatattagaaggagaagcaaaattctgtcatatgc | 539 | | | |
| Db | 581 | -TGCTACGAAAGACTTATAAGATATAAGGAGGAGCATAATTCTGTCATGAC | 639 | | | |
| OY | 540 | ttccatcaaaggcttcaatgttgcattttaaatggcataatggatc 579 | | | | |
| Db | 640 | TTCATCATATAAGCTCAGCTTGCATTTAAAGTC 679 | | | | |
| | | RESULT 12 | | | | |
| LOCUS | AA867881 | AA867881 1125 bp mRNA linear EST 16-MAR-1998 | | | | |
| DEFINITION | VX22C10_r1 | Soares_thymus_2NDMT Mus musculus cDNA clone IMAGE:2652025 similar to gb:U00978_cds1 DIHYDROLIPOAMIDE ACETYLYLTRANSFERASE COMPONENT (HUMAN); mRNA sequence. | | | | |
| VERSION | AA867881 | | | | | |
| STION | AA867881.1 | GI:2963326 | | | | |
| WORDS | EST. | | | | | |
| SOURCE | house mouse. | | | | | |
| ORGANISM | Mus musculus | | | | | |
| REFERENCE | 1 (bases 1 to 1125) | | | | | |
| AUTHORS | Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuge,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenb,K., Steppen,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R. | | | | | |
| JOURNAL | The WashU-HMU Mouse EST Project | | | | | |
| COMMENT | Unpublished (1995) | | | | | |
| | WashU-HMU Mouse EST Project | | | | | |
| FEATURES | source | Washington University School of MedicineP | | | | |
| | | 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 | | | | |
| | | Tel: 314 286 1800 | | | | |
| | | Fax: 314 286 1810 | | | | |
| | | Email: mouseest@watson.wustl.edu | | | | |
| | | This clone available royalty free through LILN ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. | | | | |
| | | MG:667754 Seq primer: -28ml3 rev2 ET from Amersham | | | | |
| | | High quality sequence stop: 494. | | | | |
| | | Location/Qualifiers | | | | |
| | | 1. .1125 | | | | |
| | | /organism="Mus musculus" | | | | |
| | | /strain="C57BL/6J" | | | | |
| | | /db_xref="taxon:10090" | | | | |
| | | /clone="IMAGE:1265202" | | | | |
| | | /clone_id="Soares_thymus_2NDMT" | | | | |
| | | /sex="male" | | | | |
| | | /tissue_type="thymus" | | | | |
| | | /lab_host="DHIOB" | | | | |
| | | /note="Vector: PTNT3D-Pac (Pharmacia) with a modified polylinker; site_1: Not I; site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTGTACCAACCTGAGTGGCGCCGGTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified PTNT3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization and was constructed by Bento Soares and M.Fatima Bonaldo." | | | | |
| BASE COUNT | 275 | a 235 c 305 g 309 t 1 others | | | | |
| ORIGIN | | | | | | |
| | | RESULT 13 | | | | |
| LOCUS | BG390485 | BG390485 664 bp mRNA linear EST 12-MAR-2001 | | | | |
| DEFINITION | 602416136F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4524345, | | | | | |
| ACCESSION | BG390485 | mRNA sequence. | | | | |
| VERSION | BG390485.1 | GI:13283933 | | | | |
| KEYWORD | EST. | | | | | |
| SOURCE | human. | | | | | |
| ORGANISM | Homo sapiens | | | | | |
| REFERENCE | 1 (bases 1 to 664) | | | | | |
| AUTHORS | NIH-MGC http://mgc.ncbi.nlm.nih.gov/. | | | | | |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | | | | |
| JOURNAL | Unpublished (1999) | | | | | |
| COMMENT | Contact: Robert Strausberg, Ph.D. | | | | | |
| | Email: cgabps-r@mail.nih.gov | | | | | |
| | Tissue Procurement: ATCC | | | | | |
| | CDNA Library Preparation: Life Technologies, Inc. | | | | | |
| | CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN) | | | | | |
| | DNA Sequencing by: Incyte Genomics, Inc. | | | | | |
| | Clone distribution: MGC clone distribution information can be | | | | | |
| | Query Match 53.2%; Score 532.4; DB 9; Length 1125; | | | | | |
| | Best Local Similarity 86.6%; Pred. No. 2.4e-127; Indels 2; Gaps 2; | | | | | |
| | Matches 609; Conservative 0; Mismatches 92; | | | | | |

LOCUS BI658188
 DEFINITION ACCESSION B1658188
 mRNA sequence.
 VERSION EST
 KEYWORDS house mouse.
 SOURCE
 ORGANISM Mus musculus
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 77)
 AUTHORS NIH-MCG <http://mgc.ncbi.nlm.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgbabs-r@mail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
 Ph.D.
 DNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM1836 row: 0 column: 23
 High quality sequence stop: 754.

| | | | |
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| QY | 421 | -caaaggaaaccataaccttattacctttcatcgatgttaatatggagaagttt | 479 |
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| QY | 596 | ttggatggacacagtataagcaaaatcatgttgtgtatgcagtggtggctcgtac | 655 |
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| Db | 686 | CCCTGCAGGACTTATACCCCTATGCTATATGCACACATAAAGGACTGGAAACAT | 745 |
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/lab_host="DH10B"
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Site:2: SALL; Cloned unidirectionally. Primer: Oligo dT.
Average insert 2.5 kb. Library constructed by Life
Technologies, catalog # 12018-016. Investigators providing
samples: Lothar Hennighausen/Priscilla Furth, NIH
Reference for transgenic model: Li et al., Cell Growth and
Differentiation 7, 3-11 (1996). Note: this is a NCBI_CGAP
Library."

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